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WHAT IS CLAIMED IS:

1. A method for predicting resistance of a pathogen to a therapeutic agent comprising:
- (a) providing a trained neural network;
 - (b) providing a determined genetic sequence from the pathogen; and
 - (c) predicting resistance of the pathogen to the therapeutic agent using the determined genetic sequence and the trained neural network.
2. The method of claim 1, wherein the pathogen is chosen from a disease-producing bacterium, a disease-producing virus, a disease-producing algae, a disease-producing fungus and a disease-producing protozoa.
3. The method of claim 2, wherein the pathogen is a disease-producing virus.
4. The method of claim 3, wherein the disease-producing virus is chosen from human immunodeficiency virus type 1, human immunodeficiency virus type 2, herpes simplex virus type 1, herpes simplex virus type 2, human papillomavirus virus, hepatitis B virus, hepatitis C virus, and Epstein-Barr virus.
5. The method of claim 4, wherein the disease-producing virus is the human immunodeficiency virus type 1.
6. The method of claim 1, wherein the trained neural network is a three-layer feed-forward neural network.
7. The method of claim 6, wherein the three-layer feed forward network comprises:
- (a) a set of input nodes, wherein each member of the set of input nodes corresponds to a mutation in the genome of the pathogen;
 - (b) a plurality of hidden nodes; and
 - (c) a set of output nodes, wherein each member of the set of output nodes corresponds to a therapeutic agent used to treat the pathogen.
8. A method for predicting resistance of a disease to a therapeutic agent comprising:
- (a) providing a trained neural network;
 - (b) providing a determined genetic sequence from the disease; and
 - (c) predicting resistance of the disease to the therapeutic agent using the determined genetic sequence and the trained neural network.

9. The method of claim 8, wherein the disease is chosen from a pathogen and a malignant cell.
10. The method of claim 9, wherein the pathogen is chosen from a disease-producing bacterium, a disease-producing virus, a disease-producing algae, a disease-producing
5 fungus, and a disease-producing protozoa.
11. The method of claim 10, wherein the pathogen is a disease-producing virus.
12. The method of claim 11, wherein the disease-producing virus is chosen from human immunodeficiency virus type 1, human immunodeficiency virus type 2, herpes simplex virus type 1, herpes simplex virus type 2, human papillomavirus virus, hepatitis
10 B virus, hepatitis C virus, and Epstein-Barr virus.
13. A method for predicting resistance of a pathogen to a therapeutic agent comprising:
15 (a) providing a neural network;
(b) training the neural network on a training data set, wherein each member of the training data set corresponds to a genetic mutation that correlates to a change in therapeutic agent resistance;
(c) providing a determined genetic sequence from the pathogen; and
(d) predicting resistance of the pathogen to the therapeutic agent using the determined genetic sequence and the trained neural network.
- 20 14. The method of claim 13, wherein the pathogen is chosen from a disease-producing bacterium, a disease-producing virus, a disease-producing algae, a disease-producing fungus and a disease-producing protozoa.
15. The method of claim 14, wherein the pathogen is a disease-producing virus.
16. The method of claim 15, wherein the disease-producing virus is chosen from
25 human immunodeficiency virus type 1, human immunodeficiency virus type 2, herpes simplex virus type 1, herpes simplex virus type 2, human papillomavirus virus, hepatitis B virus, hepatitis C virus, and Epstein-Barr virus.
17. The method of claim 16, wherein the virus is human immunodeficiency virus type 1.
- 30 18. The method of claim 13, wherein the neural network is a three-layer feed-forward neural network.

19. The method of claim 18, wherein the three-layer feed forward network comprises:
 (a) a set of input nodes, wherein each member of the set of input nodes corresponds to a mutation in the genome of the pathogen;

(b) a plurality of hidden nodes; and

5 (c) a set of output nodes, wherein each member of the set of output nodes corresponds to a therapeutic agent used to treat the pathogen.

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 10 20. A trained neural network capable of predicting resistance of a disease to a therapeutic agent, wherein the trained neural network comprises:

(a) a set of input nodes, wherein each member of the set of input nodes corresponds to a mutation in the genome of the disease; and

(b) a set of output nodes, wherein each member of the set of output nodes corresponds to the therapeutic agent used to treat the disease.

21. The trained neural network according to claim 20, wherein the disease is a pathogen.

15 22. The trained neural network according to claim 21, wherein the pathogen is chosen from a disease-producing bacterium, a disease-producing virus, a disease-producing algae, a disease-producing fungus, and a disease-producing protozoa.

23. A method of designing a therapeutic agent treatment regimen for a patient afflicted with a disease comprising:

20 (a) providing a determined genetic sequence from the disease;
 (b) inputting the determined genetic sequence into a trained neural network;
 (c) predicting resistance of the disease to a therapeutic agent using the determined genetic sequence and the trained neural network; and
 (d) using the predicted drug resistance to design the therapeutic drug
 25 treatment regimen to treat the patient afflicted with the disease.

24. The method of claim 23, wherein the disease is chosen from a pathogen and a malignant cell.

25. The method of claim 24, wherein the pathogen is chosen from a disease-producing bacterium, a disease-producing virus, a disease-producing algae, a disease-producing fungus, and a disease-producing protozoa.
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26. The method of claim 25, wherein the pathogen is a disease-producing virus.

27. The method of claim 26, wherein the disease-producing virus is chosen from human immunodeficiency virus type 1, human immunodeficiency virus type 2, herpes simplex virus type 1, herpes simplex virus type 2, human papillomavirus virus, hepatitis B virus, hepatitis C virus, and Epstein-Barr virus.

5 28. The method of claim 27, wherein the disease-producing virus is the human immunodeficiency virus type 1.

29. A method of predicting the probability of a patient developing a genetic disease comprising:

- (a) providing a trained neural network;
- 10 (b) providing a determined genetic sequence from a patient sample; and
- (c) determining the probability of the patient of developing the genetic disease using the determined genetic sequence and the trained neural network.

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